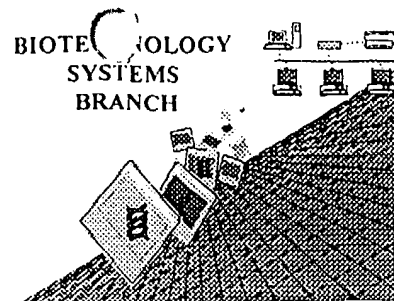


RAW SEQUENCE LISTING **ERROR REPORT**



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/602,874 A
Source: 1645
Date Processed by STIC: 2-22-01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 3.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 - 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable-form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED SUGGESTED CORRECTION

SERIAL NUMBER:

09/602-874A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ Wrapped Nucleics The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 2 ☐ Wrapped Aminos The amino acid number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".
- 3 ☐ Incorrect Line Length The rules require that a line not exceed 72 characters in length. This includes spaces.
- 4 ☒ Misaligned Amino Acid Numbering The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs between the numbering. It is recommended to delete any tabs and use spacing between the numbers.
- 5 ☐ Non-ASCII This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.
- 6 ☐ Variable Length Sequence(s) ____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and indicate in the (ix) feature section that some may be missing.
- 7 ☐ PatentIn ver. 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequence(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies primarily to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 8 ☐ Skipped Sequences (OLD RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).
- 9 ☐ Skipped Sequences (NEW RULES) Sequence(s) ____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 10 ☐ Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 11 ☐ Use of <213>Organism (NEW RULES) Sequence(s) _____ are missing this mandatory field or its response.
- 12 ☐ Use of <220>Feature (NEW RULES) Sequence(s) ____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of new Rules)
- 13 ☐ PatentIn ver. 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

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TECH CENTER
MAR 01/2900

1645

RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/602,874A
 DATE: 02/22/2001
 TIME: 09:15:18

Input Set : A:\seqlistcorr2.txt
 Output Set: N:\CRF3\02222001\I602874A.raw

**Does Not Comply
 Corrected Diskette Needed**
see pp 4, 7, 10, 11

3 <110> APPLICANT: Pompejus, Markus
 4 Kroger, Burkhard
 5 Schroder, Hartwig
 6 Zelder, Oskar
 7 Haberhauer, Gregor
 9 <120> TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING
 10 REGULATORY PROTEINS
 12 <130> FILE REFERENCE: BGI-123CP
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/09/602,874A
 C--> 15 <141> CURRENT FILING DATE: 2000-06-23
 17 <150> PRIOR APPLICATION NUMBER: 60/141031
 18 <151> PRIOR FILING DATE: 1999-06-25
 20 <150> PRIOR APPLICATION NUMBER: 60/142690
 21 <151> PRIOR FILING DATE: 1999-07-01
 23 <150> PRIOR APPLICATION NUMBER: 60/151251
 24 <151> PRIOR FILING DATE: 1999-08-27
 26 <150> PRIOR APPLICATION NUMBER: DE 19930476.9
 27 <151> PRIOR FILING DATE: 1999-07-01
 29 <150> PRIOR APPLICATION NUMBER: DE 19931419.5
 30 <151> PRIOR FILING DATE: 1999-07-07
 32 <150> PRIOR APPLICATION NUMBER: DE 19931420.9
 33 <151> PRIOR FILING DATE: 1999-07-08
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 36 <151> PRIOR FILING DATE: 1999-07-09
 38 <150> PRIOR APPLICATION NUMBER: DE 19932128
 39 <151> PRIOR FILING DATE: 1999-07-09
 41 <150> PRIOR APPLICATION NUMBER: DE 19932206.6
 42 <151> PRIOR FILING DATE: 1999-07-09
 44 <150> PRIOR APPLICATION NUMBER: DE 19932207.4
 45 <151> PRIOR FILING DATE: 1999-07-09
 47 <150> PRIOR APPLICATION NUMBER: DE 19933003.4
 48 <151> PRIOR FILING DATE: 1999-07-14
 50 <150> PRIOR APPLICATION NUMBER: DE 19941390.8
 51 <151> PRIOR FILING DATE: 1999-08-31
 53 <150> PRIOR APPLICATION NUMBER: DE 19942088.2
 54 <151> PRIOR FILING DATE: 1999-09-03
 56 <150> PRIOR APPLICATION NUMBER: DE 19942124.2
 57 <151> PRIOR FILING DATE: 1999-09-03
 59 <160> NUMBER OF SEQ ID NOS: 362

ERRORED SEQUENCES

8696 <210> SEQ ID NO: 114 (See p. 4)
 8697 <211> LENGTH: 1034
 8698 <212> TYPE: PRT
 8699 <213> ORGANISM: Corynebacterium glutamicum

RAW SEQUENCE LISTING

DATE: 02/22/2001

PATENT APPLICATION: US/09/602,874A

TIME: 09:15:19

Input Set : A:\seqlistcorr2.txt

Output Set: N:\CRF3\02222001\I602874A.raw

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8701 <400> SEQUENCE: 114
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8703 1 5 10 15
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8706 20 25 30
8708 Ala Val Glu Lys Gly Thr Phe Pro Pro Val Val Glu Gln Ile Leu Asp
8709 35 40 45
8711 Gly Lys Thr Phe Arg Ala Arg Met Asn Val His Leu Arg Thr Pro Lys
8712 50 55 60
8714 Gly Arg His Val Glu Leu Pro Thr Pro Thr Ala Ala Phe Thr Pro Glu
8715 65 70 75 80
8717 Glu Ala Val Thr Val Phe Ser Gln Leu Ser Phe Leu Lys Ala Glu Thr
8718 85 90 95
8720 Pro Ala Ala Thr Arg Ala Gln Arg Asp Ser Ile Ala Pro Asp Leu Trp
8721 100 105 110
8723 Trp Leu Ile Val Met Tyr Gln Gly Leu Ala Arg Phe Val Gln Ala Gly
8724 115 120 125
8726 Arg Val Thr Leu Arg Thr Val Met Met Asp Asn Ala Trp Trp Pro Gln
8727 130 135 140
8729 Trp Gln Leu Ser Ala Ser Leu Ser Glu Arg Gly Trp Leu Ala Glu Met
8730 145 150 155 160
8732 Asn His Ala Ala Pro Gly Ile Leu Arg Ile Asn Gly Gly Arg Asp Leu
8733 165 170 175
8735 Ala Gly Ser Met Ser Asn Glu Leu Pro His Trp Ile Ala Asn Ala Ile
8736 180 185 190
8738 Leu Arg Asp Tyr Arg Asp Glu Thr Met Pro Tyr Ala Arg His Glu Phe
8739 195 200 205
8741 Val Glu Ala Leu Leu Phe Asn His Ser Leu Arg Lys Gly Ser Thr Met
8742 210 215 220
8744 Leu Thr His Ala Leu Asn Gln Trp Lys Asn Thr Ile Thr Ser Ala Ser
8745 225 230 235 240
8747 Leu Gln Leu Val Ile Leu Val Glu Glu Pro Pro Ala Glu Ser Asp Tyr
8748 245 250 255
8750 Glu Asp Pro Met Asp Ser Val Trp Pro Val Arg Leu Met Val Arg Thr
8751 260 265 270
8753 Gly Val Asp Ala Pro Gln Ala Ile Gln Lys Gly Ser Ile Asp Ser Gly
8754 275 280 285
8756 Gly Met Glu Gln Leu Arg Ser Gln Tyr Glu Thr Ala Lys Thr Thr Ser
8757 290 295 300
8759 Met Leu Leu Asp Pro Ala Arg Glu Asp Ala Met Leu Gly His Met Val
8760 305 310 315 320
8762 Asp Ile Ala Gln Asn Gly Asp Trp Asp Ile Phe Leu Thr Thr Glu Glu
8763 325 330 335
8765 Ile Val Asn Phe Ile Ser His Asp Val Ala Lys Leu Arg Lys Ala Gly
8766 340 345 350
8768 Ile Pro Val Met Leu Pro Lys Ala Trp Ser Thr Tyr Glu Thr Arg Ala
8769 355 360 365
8771 Gln Val Glu Ala Arg Thr Pro Asn Asp Ala Ala Asp Ser Ser Thr Lys
8772 370 375 380

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RAW SEQUENCE LISTING

DATE: 02/22/2001

PATENT APPLICATION: US/09/602,874A

TIME: 09:15:19

Input Set : A:\seqlistcorr2.txt

Output Set: N:\CRF3\02222001\I602874A.raw

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8774 Ala Ile Ile Gly Leu Asp Gln Leu Val Glu Tyr Asn Trp Arg Ile Ser
8775 385 390 395 400
8777 Val Gly Asp Ile Gln Leu Ser Asp Glu Glu Met Arg Glu Leu Ile Asp
8778 405 410 415
8780 Ser Lys Thr Gly Leu Ile Arg Leu Arg Gly Asp Trp Val Met Ala Asp
8781 420 425 430
8783 Gln Asp Ala Leu Arg Arg Ile Thr Ser Tyr Met Glu Glu Leu Ser Lys
8784 435 440 445
8786 Ser Ser Glu Lys Arg Ala Arg Thr Glu Met Glu Lys Val Ala Met Gln
8787 450 455 460
8789 Ala Lys Leu Ala Glu Ala Asn Gly Glu Glu Gly Trp Gln Leu Leu Ala
8790 465 470 475 480
8792 Ala Lys Ala Glu Thr Leu Arg Lys Glu Phe Asn Glu Lys Phe Ser Gly
8793 485 490 495
8795 Asp Gly Gln Gly Glu Val Thr Leu Ala Glu Leu Arg Glu Ile Ala Leu
8796 500 505 510
8798 Lys Ala Ala Glu Asn Glu Pro Val Glu Phe Thr Gly Ser Gln Trp Phe
8799 515 520 525
8801 Asn Ser Leu Leu Gly Gly Thr Glu Thr Pro Ala Pro Val Arg Val Asp
8802 530 535 540
8804 Ile Pro Asp Thr Val Leu Ala Asp Leu Arg Glu Tyr Gln Arg Arg Gly
8805 545 550 555 560
8807 Val Asp Trp Leu Tyr Trp Met Ser Ala Asn Asn Leu Gly Ala Val Leu
8808 565 570 575
8810 Ala Asp Asp Met Gly Leu Gly Lys Thr Leu Gln Leu Leu Ser Leu Leu
8811 580 585 590
8813 Ala Val Glu Arg Ala Glu Asn Pro Glu Leu Glu Arg Gly Pro Thr Leu
8814 595 600 605
8816 Val Val Cys Pro Thr Ser Val Val Gly Asn Trp Ala Ala Glu Ala Ala
8817 610 615 620
8819 Lys Phe Val Pro Ser Leu Lys Val Leu Met His His Gly Pro Gln Arg
8820 625 630 635 640
8822 Leu Asn Asp Ala Asp Phe Leu Ser Gln Ser Lys Gly Met Asp Leu Ile
8823 645 650 655
8825 Ile Thr Ser Tyr Gly Val Ile Thr Arg Asp Phe Lys Leu Met Gly Gln
8826 660 665 670
8828 Val Gly Phe Glu Arg Val Val Leu Asp Glu Ala Gln Ala Ile Lys Asn
8829 675 680 685
8831 Ser Ser Thr Arg Val Ser Lys Ala Val Arg Ser Leu Pro Ser Arg His
8832 690 695 700
8834 Arg Val Ala Leu Thr Gly Thr Pro Val Glu Asn Arg Leu Ser Glu Met
8835 705 710 715 720
8837 Arg Ser Ile Leu Asp Phe Cys Asn Pro Gly Val Leu Gly Ser Ala Ser
8838 725 730 735
8840 Phe Phe Arg Asn His Phe Ala Lys Ala Ile Glu Arg Glu Gln Asp Asp
8841 740 745 750
8843 Thr Met Thr Glu Arg Leu Arg Gln Leu Thr Ala Pro Phe Ile Leu Arg
8844 755 760 765
8846 Arg Leu Lys Thr Asp Pro Asn Ile Ile Asp Asp Leu Pro Glu Lys Thr

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RAW SEQUENCE LISTING
 PATENT APPLICATION: US/09/602,874A
 DATE: 02/22/2001
 TIME: 09:15:19

Input Set : A:\seqlistcorr2.txt
 Output Set: N:\CRF3\02222001\I602874A.raw

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8847      770      775      780
8849 Glu Gln Ile Ile Arg Val Asp Met Thr Thr Glu Gln Ala Ser Leu Tyr
8850 785      790      795      800
8852 Lys Ala Leu Val Glu Asp Val Gln Lys Gln Leu Asp Glu Arg Gln Gly
8853      805      810      815
8855 Met Ser Arg Lys Gly Leu Val Leu Ala Thr Ile Thr Arg Ile Lys Gln
8856      820      825      830
8858 Ile Cys Asn His Pro Ala His Phe Leu Gly Asp Gly Ser Glu Val Thr
8859      835      840      845
8861 Leu Lys Gly Lys His Arg Ser Gly Lys Val Glu Ala Leu Met Glu Leu
8862      850      855      860
8864 Ile Asp Thr Ala Val Lys Glu Glu Arg Arg Met Leu Ile Phe Thr Gln
8865 865      870      875      880
8867 Tyr Ala Ala Phe Gly Arg Ile Leu Ala Pro Tyr Leu Ser Asp Arg Leu
8868      885      890      895
8870 Gly Thr Asn Ile Pro Phe Leu His Gly Gly Val Thr Lys Pro Gly Arg
8871      900      905      910
8873 Asp Arg Met Val Ala Glu Phe Gln Ser Glu Asp Gly Pro Pro Ala Met
8874      915      920      925
8876 Ile Leu Ser Leu Lys Ala Gly Gly Thr Gly Leu Asn Leu Thr Ala Ala
8877      930      935      940
8879 Ser Ile Val Val His Met Asp Arg Trp Trp Asn Pro Ala Val Glu Asn
8880 945      950      955      960
8882 Gln Ala Thr Asp Arg Ala Phe Arg Ile Gly Gln Arg Lys Asn Val Asp
8883      965      970      975
8885 Val Tyr Lys Met Ile Thr Val Gly Thr Met Glu Glu Ser Ile Gln Asp
8886      980      985      990
8888 Ile Leu Asp Gly Lys Thr His Leu Ala Ser Ala Ile Val Glu Glu Gly
E--> 8889      995      1000      1005
E--> 8892      1010      1015      1020
8894 Ser Tyr Arg Glu Lys Glu Gly Ala Asp Asp
8895 1025      1030
20702 <210> SEQ ID NO: 284
20703 <211> LENGTH: 1124
20704 <212> TYPE: PRT
20705 <213> ORGANISM: Corynebacterium glutamicum
20707 <400> SEQUENCE: 284
20708 Met Pro Ala Gly Ile Ala Asp Met Thr Asp Ser Leu Leu Gly Trp Ala
20709 1 5 10 15
20711 Ser Gln Thr Glu Leu Asp Leu Asn Gln Arg Leu Ala Gly Val Glu Tyr
20712 20 25 30
20714 Phe Pro Gln Ile Gln Leu Arg His Asp Glu Leu Glu Arg Ile His Arg
20715 35 40 45
20717 Phe Tyr Gly Thr Phe Leu Ser Arg Gln Val Gly Ala Gly Ala Ser Leu
20718 50 55 60
20720 Gly Asp Leu Phe Glu Met Thr Pro Cys Leu Thr Val Thr Thr Leu Val
20721 65 70 75 80
20723 Ser Arg Ala Ser Arg Ile Ser Asp Pro Ala Asp Phe Phe Gly Glu Tyr

```

Val
1005

misaligned amino acid
 numbering. Adjust circled
 numbers to the left.
 There must be no
 numbers with digits
 under two amino
 acids.

See # 4 on
 Error Summary
 Sheet

RAW SEQUENCE LISTING

DATE: 02/22/2001

PATENT APPLICATION: US/09/602,874A

TIME: 09:15:21

Input Set : A:\seqlistcorr2.txt

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20724		85		90		95
20726	Ile Gly Gly Leu Ser Ala Glu His Ala Ala Val Val Glu Gly					
20727		100		105		110
20729	Leu Thr Glu Lys Leu Phe Ala Gln Ala Gly Leu Leu Val Pro Glu Gly					
20730		115		120		125
20732	Ile Ala Ser Pro Leu Glu Leu Ser Ile His Ala Gly Ile Ser Asn					
20733		130		135		140
20735	His Glu Val Ala Ala Val Leu Thr Glu Val Glu Asn Gly Thr Thr Glu					
20736		145		150		155
20738	Tyr Pro Phe Met Phe Asp Ala Val Leu Arg Leu Thr Pro Glu Trp Ala					
20739		165		170		175
20741	Gln Thr Leu Ile Gly Gly Val Gln Glu Leu Ile Glu Phe Ala Thr Thr					
20742		180		185		190
20744	His Arg Thr Ser Trp Ser Asp Arg Gln Arg Glu Ser Ser Leu Pro Ala					
20745		195		200		205
20747	Met Ile Asp Glu Ile Val Val Ala Glu Leu Arg Glu Arg Pro Val Gly					
20748		210		215		220
20750	Thr Ala Asp Arg Glu Asn Ser Val Gly Val Ala Leu Arg Glu Leu Arg					
20751		225		230		235
20753	Pro Arg Leu Ile Leu Asp Ala Glu Arg Arg Lys Val Cys Leu Arg Leu					
20754		245		250		255
20756	Pro Glu Gln Arg Val Ser Asp Asp Glu Ile Asn Trp Arg Val Ser Leu					
20757		260		265		270
20759	Glu Gly Thr Thr Arg Ile Phe Ser Thr Arg Arg Ala Trp Gly Asp Thr					
20760		275		280		285
20762	Ser Gly Tyr Ser Glu Ala Leu Asp Ile Thr Val Glu Arg Gln Ile Arg					
20763		290		295		300
20765	Glu Thr Thr Val Thr Asp Thr Ser Asn Gln Ile Thr Trp Val Val Pro					
20766		305		310		315
20768	Val Val Asp Phe Asn Asp Pro Val Leu Val Phe Ser Ala Arg Gly Glu					
20769		325		330		335
20771	Asn Leu Thr Asp Lys Val Ser Leu His His Gln Glu Ile Tyr Val Leu					
20772		340		345		350
20774	Ala Pro Ala Glu Ala Lys Leu Glu Asp Met Val Thr Gly Gln Pro Val					
20775		355		360		365
20777	Pro Val Ile Glu Gln Phe Leu Val Glu Gly Trp Asn Ser Trp Val Cys					
20778		370		375		380
20780	Ser Arg Val Asp Ala Arg Gly Leu Ser Ser Leu Lys Val Asn Lys Glu					
20781		385		390		395
20783	Val Arg Cys Ile Asp Pro Arg Arg Arg Val Ala Phe His His Pro Ala					
20784		405		410		415
20786	Glu Leu Val Pro His Val Arg Ser Ile Ser Gly Leu Pro Val His Ala					
20787		420		425		430
20789	Gln Ser Leu Ile Ala Glu Phe Pro Pro Thr Leu Ser Gly Gln Asp Glu					
20790		435		440		445
20792	Thr Trp Met Leu Ser Ile Ser Ala Phe Ala Gly Val Gly Ala Ala Gly					
20793		450		455		460
20795	Glu Glu Ile Ala Glu Pro Glu Pro Leu Glu Val Pro Ala Asp Gly Gly					
20796		465		470		475
						480

RAW SEQUENCE LISTING

DATE: 02/22/2001

PATENT APPLICATION: US/09/602,874A

TIME: 09:15:21

Input Set : A:\seqlistcorr2.txt

Output Set: N:\CRF3\02222001\I602874A.raw

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20798 Leu Phe Ala Ile Phe Asp Pro Glu Ile Tyr Asp Ala Pro Trp Val Gly
20799                               485                               490                               495
20801 Glu Tyr Leu Val Arg Leu Arg Gly Pro Arg Asn Glu Ser Phe Arg Pro
20802                               500                               505                               510
20804 Glu Phe Ala Ile Val Glu Asp Met Thr Thr Glu Phe Glu Val Ala Ser
20805                               515                               520                               525
20807 Gly Ala Ser Phe Arg Ile Pro Thr Thr Thr Gly Leu Ser Glu Ala Ser
20808                               530                               535                               540
20810 Leu Arg Val Arg Ser Gly Glu Lys His Phe Thr Ala Glu Pro Arg Leu
20811 545                               550                               555                               560
20813 Val Thr Val Glu Ala Thr Asp Pro Asn Ala Ser Phe Val Val Thr Thr
20814                               565                               570                               575
20816 Asp Glu Gly Asp Gln Met Pro Leu Arg Phe Val Pro Pro Gln Ile Ala
20817                               580                               585                               590
20819 Ile Glu Leu Pro Leu Thr Thr Glu Pro Pro Thr Trp Arg Val Thr Arg
20820                               595                               600                               605
20822 Thr Val Cys Gly Pro Arg Asp Leu Asp Gly Ala Gly Glu Leu Arg Ile
20823 610                               615                               620
20825 Arg Thr Gly Val Asp Val Gly Asp Pro Lys Val Ser Val Arg Asn His
20826 625                               630                               635                               640
20828 His Gly Ser Pro Leu Arg Thr Val Lys Met Val Thr Pro Asp Asn Gly
20829                               645                               650                               655
20831 Arg Thr Trp Ile Ala Ser Met Lys Glu Ile Ala Ala Ser Thr Phe Val
20832                               660                               665                               670
20834 Met Pro Arg Gly Ser Ile Glu Phe Glu Trp Thr Asp Arg Lys Val Asp
20835 675                               680                               685
20837 Arg Arg Val Ser Val Thr Ile Ala Val Ile Asp Lys Thr Glu Asn Phe
20838 690                               695                               700
20840 Thr Gly Ile Thr Ile Glu Asp Gly Lys Leu Val Phe Glu Glu Leu Ala
20841 705                               710                               715                               720
20843 Ala Gly Arg Gln Leu Ala Ala Trp Val Trp Pro Gln Thr Ala Pro Trp
20844                               725                               730                               735
20846 Val Ser Ala Val Glu Leu Ala Val Thr Gly Pro Glu Leu Glu Leu Pro
20847 740                               745                               750
20849 Glu Val Leu Val Gly Ala Gly Asn Leu Ile Val Gln Leu His Thr Ala
20850 755                               760                               765
20852 Asp Pro Phe Thr Thr Ser Val Thr Pro Leu Ser Pro Gly Lys Ala Ala
20853 770                               775                               780
20855 Val Thr Val Glu Gln Glu Gly Tyr Tyr Ser Ala Gln Thr Glu Glu Tyr
20856 785                               790                               795                               800
20858 Ala Gln Leu Ser Ala Phe Phe Gly Gly Glu Val Glu Glu Pro Pro Ile
20859 805                               810                               815
20861 Ser Asp Ala Val Val Pro Ala Leu Trp Asp Val Ser His Ile Trp Thr
20862 820                               825                               830
20864 Glu Gln Gly Asn Thr Glu His Leu Pro Val Val His Ala Ala Leu Arg
20865 835                               840                               845
20867 Ser Ser Pro Ala Ala Ala Leu Lys Gly Leu Ser Ala Ser Leu Val Pro
20868 850                               855                               860
20870 Ala Gln Ala Leu Pro Gly Lys Val Ile Ser Ser Gly Leu Ala Ala Ser

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RAW SEQUENCE LISTING

DATE: 02/22/2001

PATENT APPLICATION: US/09/602,874A

TIME: 09:15:21

Input Set : A:\seqlistcorr2.txt

Output Set: N:\CRF3\02222001\I602874A.raw

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20871 865      870      875      880
20873 Pro Phe Thr Thr Glu Ser Pro Ala Thr Glu Val His Arg Thr Ala Trp
20874      885      890      895
20876 Ile Gly Thr Leu Gln Leu Leu Gly Ala Leu Pro Ser Ala Phe Lys Glu
20877      900      905      910
20879 Ala Glu Glu Leu Gly Asn Arg Thr Pro Leu Leu Pro Ile Leu Gly Gln
20880      915      920      925
20882 Leu Glu Glu Val Ala Gly Lys Asn Ile Leu Ser Thr Leu Ala Thr Gly
20883      930      935      940
20885 Arg Asp Ser Thr Leu Asp Thr Ala Cys Ile Asp Gln Ser Thr Val Ala
20886 945      950      955      960
20888 Ile Ala Gly Met Asn Glu Thr Gln Gln Lys Ala Leu Leu Asp Met Phe
20889      965      970      975
20891 Phe Ser Asn Ala Asp Ile Val Pro Gly Pro Leu Met Glu Asp Asn Thr
20892      980      985      990
20894 Arg Leu Met Ala Val Phe Glu Thr Phe Lys Lys Arg Asp Ala Leu Arg
E--> 20895 995      1000      1005
20897 Glu Val Leu Gln Thr Glu Gly Leu Ile Lys Thr Ala Val Glu Leu Leu
E--> 20898 1010      1015      1020
20900 Arg Ala Met Arg Gly Thr Gln Arg Gln Leu Tyr Ser Ser Ala Arg Ile
E--> 20901 1025      1030      1035      1040
20903 Arg Phe Asp Lys Leu Asp Gly Val Asn Thr Asp Asn Pro Glu Asn Met
E--> 20904      1045      1050      1055
20906 Trp Ala Leu Thr Pro Val Val Ser Leu Val Phe Ala Leu Ser Ser Arg
E--> 20907      1060      1065      1070
20909 Leu His Ala His Glu Leu Ile Gly Lys Thr Arg Thr Leu Asp Arg Ala
E--> 20910      1075      1080      1085
20912 Ser Ala Gly Trp Gly Arg Ile Ala Asp Leu Val Pro Asp Leu Val Thr
E--> 20913 1090      1095      1100
20915 Gly Asp Leu Ile Ser Ala Glu Ala Met Val Leu Gly Ala Arg Asn Pro
E--> 20916 1105      1110      1115      1120
20918 Gly Leu Val Asp
21352 <210> SEQ ID NO: 288
21353 <211> LENGTH: 1233
21354 <212> TYPE: PRT (See p. 10)
21355 <213> ORGANISM: Corynebacterium glutamicum
21357 <400> SEQUENCE: 288
21358 Val Thr Ile Ser Arg Arg Leu Lys Gln Glu Arg Ser Phe Ala Asp Asp
21359 1 5 10 15
21361 Leu Gln Asp Leu Lys Thr Leu Asn Asp Gln Leu Arg Phe Thr Asn Ala
21362 20 25 30
21364 Lys Leu Gln Ala Arg Ile Ser Gly Ile Gly Asn Asp Gly Lys Lys Ile
21365 35 40 45
21367 Thr Arg Pro Thr Pro Leu Leu Ala Leu Asp Phe Gln Leu Thr Val Glu
21368 50 55 60
21370 Glu Tyr Glu Thr Ile Ile Ala Ile Leu Val Glu Ala Val Gly Gly Asn
21371 65 70 75 80
21373 Gln Ser Lys Pro Ala Ile Leu Lys Asp Leu Phe Ile Glu Tyr Pro Leu
21374 85 90 95

```

Ile
1040
misaligned amino
acid numbers. Refer
to explanation on
p. 4.

Pro
1120

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/602,874A

DATE: 02/22/2001

TIME: 09:15:22

Input Set : A:\seqlistcorr2.txt

Output Set: N:\CRF3\02222001\I602874A.raw

```

21376 Val Phe Leu Ala Ala Leu Ser Gly Thr Ala Met Leu Asp Ala Gln Glu
21377      100      105      110
21379 Gly Phe Trp Pro Ala Phe Trp Lys Arg Thr Gln Val Ser Val Pro Glu
21380      115      120      125
21382 His Val Tyr Asp Ala Ile Arg Lys Glu Leu Val Asn Ser Ile Arg Lys
21383      130      135      140
21385 Asn Gly Leu Glu Thr Phe Ser Leu Ala Asp Leu Asn Arg Arg Glu Tyr
21386      145      150      155      160
21388 Val Gly Leu Ile Gln Leu His Ser Gly Leu Ser Ala Lys Asp Met Leu
21389      165      170      175
21391 Ala Leu Val Lys Phe Ile Asp His Thr Arg Ala Glu Asn Gln Gly Trp
21392      180      185      190
21394 Asp Ser Gly Glu Asp Phe Ala Ser Tyr Ala Lys Ser Val Phe Ser Ser
21395      195      200      205
21397 Gly Asp Asn Leu Leu Thr Thr Glu Ser Leu Lys Gln Leu Val Thr His
21398      210      215      220
21400 Ile Pro Ala Arg Ser Val Asp Phe Ile Ala Arg Val Tyr Glu Leu Thr
21401      225      230      235      240
21403 Asn Trp Tyr Arg Asp Leu Lys Asp Leu Asn Glu Val Glu Ala Phe Val
21404      245      250      255
21406 Gly Thr His Gly Leu Pro Glu Leu Ser Phe Lys Phe Leu Leu Glu Cys
21407      260      265      270
21409 Leu Ser Gly Glu Ala Glu Gln Ile Ala Glu Lys Thr Lys Ala Ala Pro
21410      275      280      285
21412 Ala Ser Leu Glu Asn Leu Glu Pro Pro His Leu Tyr Leu Asp Pro Gln
21413      290      295      300
21415 Ser Phe Glu Leu Ser Leu Val Phe Pro Ala Ile Ser Lys Thr Ala Ala
21416      305      310      315      320
21418 Leu Gln Ile Pro Ala Pro Glu Trp Thr Val Ile Tyr Asp Gly Asn Ser
21419      325      330      335
21421 Ile Lys Val Arg Pro Glu Gln Asp Trp Ser Tyr Gly Gly Phe Ala Glu
21422      340      345      350
21424 Tyr Arg Leu Pro Leu Asp Lys Pro Leu Ser Ser Leu Arg Val Ile Thr
21425      355      360      365
21427 Pro Thr Glu Lys Ser Leu Ile Leu Ile Glu Gly Phe Gly His Lys Asn
21428      370      375      380
21430 Pro Ile Met Phe Phe Lys Asn Asn Gly Gln Pro Tyr Ala Asn Gln Glu
21431      385      390      395      400
21433 Met Leu Ser Gly Asn Ala Val Thr Ala Ile Val Pro Ala Ala Ala Ile
21434      405      410      415
21436 Ile Arg Ala Arg Met Arg Ala Ser Lys Thr Phe Asn Tyr Gln Asp Leu
21437      420      425      430
21439 Gly Pro Leu Ser Gly Trp Asn Lys Trp Val Ile Arg Ser Ile Pro Leu
21440      435      440      445
21442 Lys Arg Ala Glu Ser Ile Thr Val Ser His Gly Gly Phe Arg Lys Glu
21443      450      455      460
21445 Leu Pro Val Arg Arg Lys Val Asp Val Gln Trp Ile Thr Glu Asp Leu
21446      465      470      475      480
21448 Thr Ile Glu Asn Leu Gln Gly Leu Asp His Glu Pro Val Phe His Thr

```

RAW SEQUENCE LISTING

DATE: 02/22/2001

PATENT APPLICATION: US/09/602,874A

TIME: 09:15:22

Input Set : A:\seqlistcorr2.txt

Output Set: N:\CRF3\02222001\I602874A.raw

```

21449          485          490          495
21451 Ser Pro Arg Ile Glu Phe Pro Thr Ser Gly Ser Asn Trp Val Ile Gln
21452          500          505          510
21454 Tyr Ser Gln Ile Leu Pro Asp Gly Ser Leu Ile Glu Met Glu Asp Tyr
21455          515          520          525
21457 Pro Val Glu Pro Glu Asn Phe Gly Tyr Glu Leu Asp Leu Phe Glu Glu
21458          530          535          540
21460 Ser Asp Asp Pro Trp Val Gly Gln Phe Leu Val Thr Leu Leu Lys Asp
21461 545          550          555          560
21463 Glu Lys Val Tyr Glu Thr Arg Lys Phe Asn Leu Ala Glu Gly Leu Asp
21464          565          570          575
21466 Leu Ser Leu Thr Phe Ser Gly Gly Gly Pro Glu Asn Arg Phe Arg Tyr
21467          580          585          590
21469 Pro Ser Ile Asn Gln Gly Gln Thr Gly Leu Thr Lys Thr Phe Ala Arg
21470          595          600          605
21472 Phe Ser Ser Asn Ser Glu Lys His Ile Arg Phe Pro Asp Glu Ile Ile
21473          610          615          620
21475 Gly Leu Asp Ala Phe Thr Ser Gln Lys Ala Phe Asn Ile Ala Ser Gly
21476 625          630          635          640
21478 Asp Phe Pro Glu Asp Tyr Asn Leu Asp Val Phe Ile Thr Pro Pro Gln
21479          645          650          655
21481 Leu His Tyr Gln Val Pro Val Thr His Ser Gln Thr Lys Trp Glu Ser
21482          660          665          670
21484 Thr Lys Thr Thr Leu Asp Phe Asn Asp Phe Ala Asp Gly Asn Leu Gln
21485          675          680          685
21487 Ile Arg Phe Pro Asn Glu Val Tyr Asp Pro Asn Leu Lys Ile Ile Lys
21488          690          695          700
21490 Met Val Ala Tyr Lys Lys Pro Glu Ser Ser Glu Pro Lys Tyr Leu Ser
21491 705          710          715          720
21493 Lys Ile Gly Ser Ser Lys Val Trp Ser Ile Pro Met Asp Arg Ile Lys
21494          725          730          735
21496 Glu Leu Met Asp Asp Asp Ala Gln Phe Leu Leu Ile Ala Glu Trp Phe
21497          740          745          750
21499 Ala Glu Ser Lys Asp Gln His Arg Glu Lys Ile Ile Ser Glu Ala Lys
21500          755          760          765
21502 Arg Thr Gly Lys Ile Ser Asn Ala Ala Leu Lys Ser Ala Arg Pro Gln
21503          770          775          780
21505 Pro Gln Ala Ser Ser His Ile Ala Thr Ile Glu Lys Lys Pro Leu Leu
21506 785          790          795          800
21508 Ala Ala Ala Glu Ile Lys Leu Ser Thr Val Glu Leu Glu Leu Gly Arg
21509          805          810          815
21511 His Thr Ser Lys Arg Leu Glu Gly Trp Ala Trp Ser Ala Leu Asn Pro
21512          820          825          830
21514 Leu Asp Pro Pro Ile Lys Val Asp Phe Gln Gly Thr Ser Gly Ser Leu
21515          835          840          845
21517 Pro Asp Thr His Phe Val Val Gly Pro Leu Ile Val Glu Val Arg Glu
21518          850          855          860
21520 Lys Glu Phe Leu Ser Gln Trp Gln Pro Lys Val Pro Ser Val Lys Ala
21521 865          870          875          880

```

RAW SEQUENCE LISTING

DATE: 02/22/2001

PATENT APPLICATION: US/09/602,874A

TIME: 09:15:22

Input Set : A:\seqlistcorr2.txt

Output Set: N:\CRF3\02222001\I602874A.raw

```

21523 Val Val Ala Asn Asp Pro Ser Phe Glu Leu Asp Pro Gln Phe Asp Pro
21524          885          890          895
21526 Phe Leu Thr His Arg Trp Met Phe Ala Pro Arg Ser Gly Lys Val Leu
21527          900          905          910
21529 Leu Pro Gln Glu Ile Arg Thr Val Trp Asp Ala Arg Phe Asn Met Arg
21530          915          920          925
21532 His Val Leu Ala Gln Arg Glu Asn Leu His Val Lys Ser Ile Gln Asp
21533          930          935          940
21535 Phe Asp Asp Ala Thr Ser Thr Tyr Leu Thr Ser Asp Pro Arg Val Ala
21536 945          950          955          960
21538 Leu Asp Glu Leu Asp Lys Ser Ser Ile Pro Ser Asn Ser His Phe Glu
21539          965          970          975
21541 Ser Phe Ile Arg Ser Gly Leu Ala Glu Leu Ser Phe Glu Val Asp Asp
21542          980          985          990
21544 Thr Ala Gly Asp Ile His Arg Val Pro Trp Ile Gly Leu Ile Gln Glu
E--> 21545 995          1000          1005
21547 Met Asn Asp Leu Arg Ile Leu Gln Ile Gln Gly Tyr Glu Thr Glu Glu
E--> 21548 1010          1015          1020
21550 Arg Ala Ile Glu Arg Arg Asn Ser Gln Ser Tyr Ile Arg Glu Ile Gly
E--> 21551 1025          1030          1035          1040
21553 Gly Ser Glu Leu Trp Asn Ile Leu Lys Gly Asn Ser Glu Gly Leu Ser
E--> 21554          1045          1050          1055
21556 Leu Ala Gln Lys Cys Ala Pro Gln Ala Thr Glu Ile Asn Val Ile Arg
E--> 21557          1060          1065          1070
21559 Asn Ser Gly Leu Glu Ala Met Arg Asn Gly Leu Gly Ala Asp Gln Phe
E--> 21560          1075          1080          1085
21562 Ser Ala Glu Phe Ile Ser Ala Asp Ser Arg Leu Arg Ala Gln Leu Glu
E--> 21563          1090          1095          1100
21565 Trp Leu Glu Asn Arg Arg Glu Leu Asn Asp Leu Gly Glu Leu Pro Thr
E--> 21566 1105          1110          1115          1120
21568 Leu Phe Asp Phe Ala Glu Lys Tyr Glu Tyr Leu Ile Asp His Leu Gly
E--> 21569          1125          1130          1135
21571 Asp Asp Arg Ile Lys Val Thr Ala Arg Glu Leu Ser Thr Leu Ala Ser
E--> 21572          1140          1145          1150
21574 Glu His Arg Arg Gly Asn Ala Glu Asn Trp Leu Tyr Ala Pro Tyr Val
E--> 21575          1155          1160          1165
21577 Ser Phe Ile Tyr Ser Leu Leu Asn Arg Met Ile Ala His Glu Val Ile
E--> 21578          1170          1175          1180
21580 Arg Pro Ile Ala Gln Ile Asn Tyr Ser Arg His Asp Trp Ala Asn Ala
E--> 21581 1185          1190          1195          1200
21583 Ala Arg Leu Ile Pro Arg Leu Thr Gly Phe Asp Leu Val Ser Ala Glu
E--> 21584          1205          1210          1215
21586 Ala Lys Val Leu Ser Ala Ile Asn Asn Asn Ile Ile Pro Thr Ala
E--> 21587          1220          1225          1230
21589 Ile
26414 <210> SEQ ID NO: 362
26415 <211> LENGTH: 17
26416 <212> TYPE: DNA
26417 <213> ORGANISM: Artificial Sequence

```

*Misaligned amino
acid numbering. Refer
to p. 4.*

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/602,874A

DATE: 02/22/2001
TIME: 09:15:23

Input Set : A:\seqlistcorr2.txt
Output Set: N:\CRF3\02222001\I602874A.raw

26419 <220> FEATURE:
26420 <223> OTHER INFORMATION: Description of Artificial sequence: Primer
26422 <400> SEQUENCE: 362

E--> 26423 gtaaaacgac ggccagt
W--> 26425 BGI-123CP - 434 -

18

17 bases shown

→ Delete end of file material. It
is causing an invalid base count for
Sequence # 362.

VERIFICATION SUMMARY

DATE: 02/22/2001

PATENT APPLICATION: US/09/602,874A

TIME: 09:15:24

Input Set : A:\seqlistcorr2.txt

Output Set: N:\CRF3\02222001\I602874A.raw

L:14 M:270 C: Current Application Number differs, Replaced Application Number
L:15 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:8685 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:113
L:8689 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:113
L:8889 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:114
M:332 Repeated in SeqNo=114
L:20669 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20673 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20677 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20681 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20685 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20689 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20693 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20697 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:283
L:20895 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:284
M:332 Repeated in SeqNo=284
L:21291 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21295 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21299 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21303 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21307 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21311 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21315 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21319 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21323 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21327 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21331 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21335 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21339 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21343 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:287
L:21545 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:288
M:332 Repeated in SeqNo=288
L:26423 M:254 E: No. of Bases conflict, LENGTH:Input:18 Counted:17 SEQ:362
L:26425 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:4